

10/009962

Fig. 1

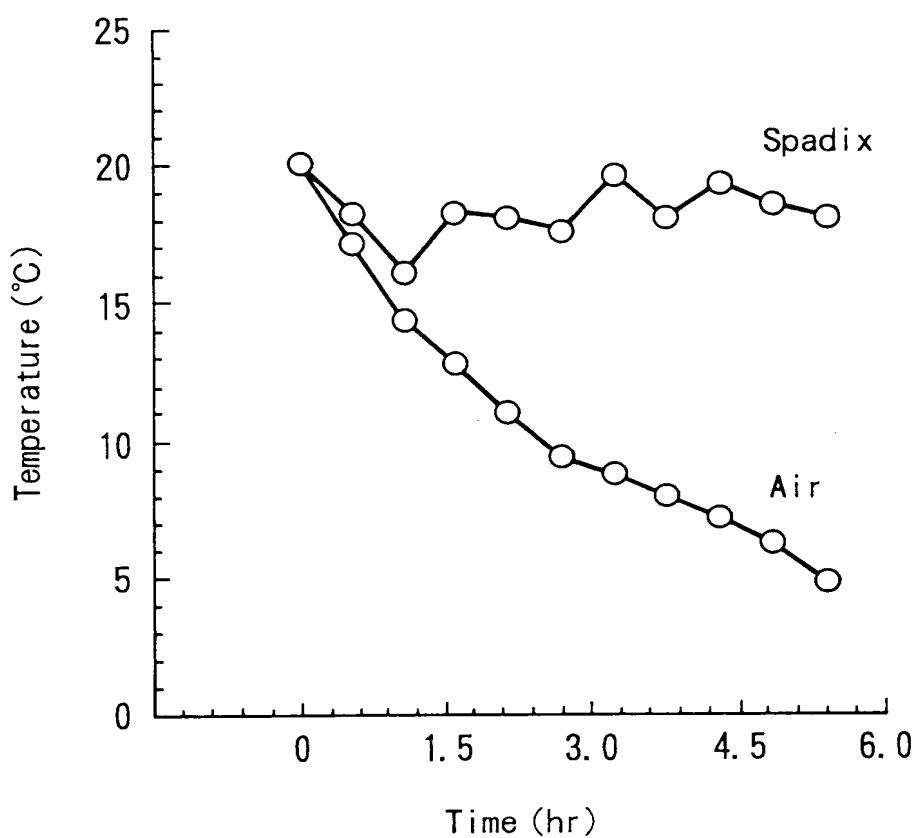


Fig. 2

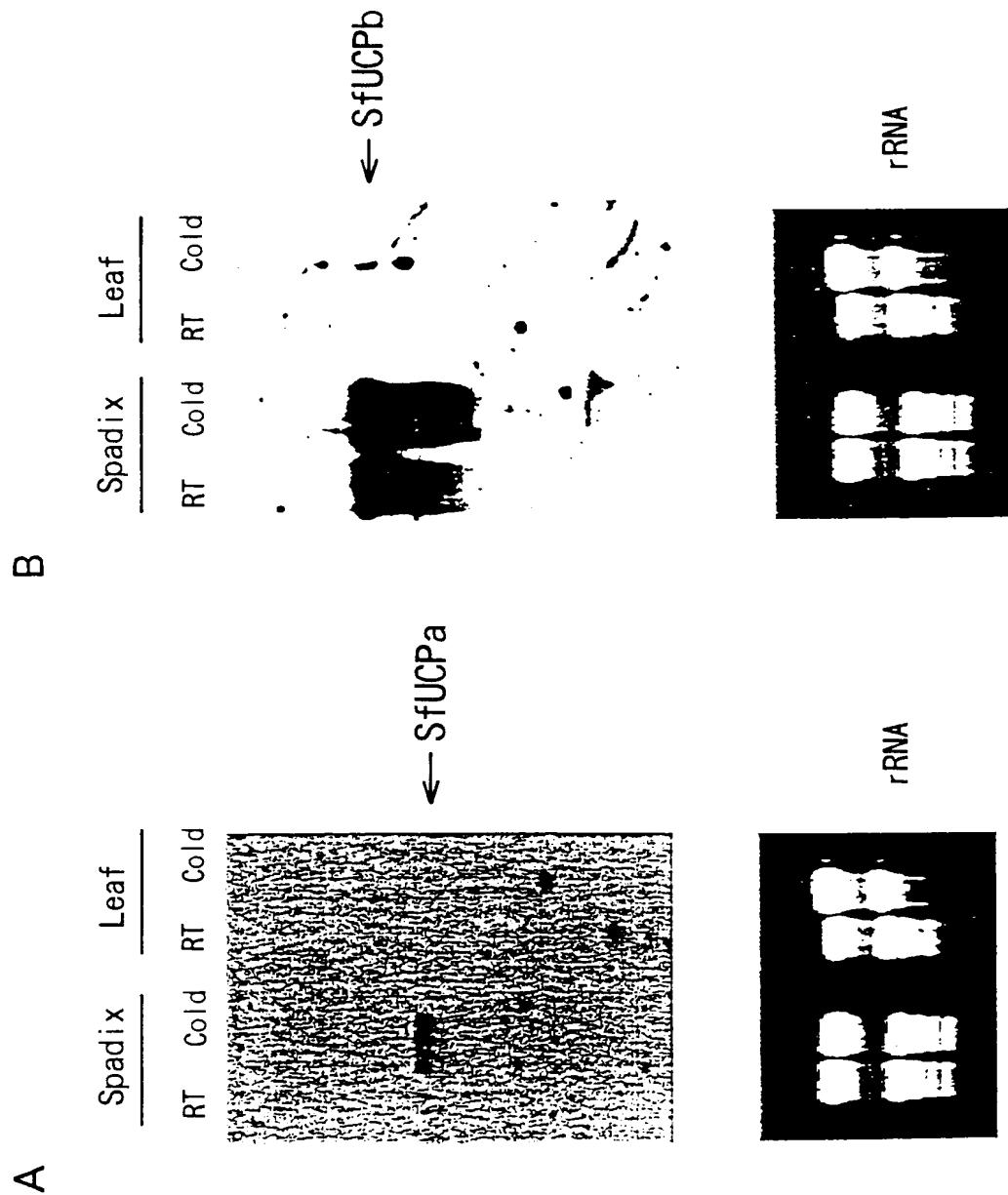


Fig. 3 Top

		I		II
SfUCPA	1	--MGDHGPRTEISFAGSSR-AAFAACFAELCT	PLOTAKVRQLQKRAVITGDV-VALPKY	56
SfUCPB	1	--MGDHGPRTEISFAGSSR-AAFAACFAELCT	PLOTAKVRQLQKRAVITGDV-VALPKY	56
StUCP	1	MCGGDHGCKSDISFAGIFASSAAACFAEACTI	PLOTAKVRQLQKRAVEGDG-LALPKY	59
AtPUMP	1	--MVAAGKSDLSLPKTFACSAFAACVGEVCTI	PLOTAKVRQLQKSAFTLAGDVTLPKY	57
human UCP1	1	-MGGLTASDVRHPTLGVQLFSAPIAACIADVI	TPLDTAKVRQLQVQGECP---TSSVIRY	55
human UCP2	1	-KVGFKAATDVPPTATVKFLGACTAACIADLITP	PLOTAKVRQLQIIGESSQGPVRATASAQY	59
human UCP3	1	-KVGLKPSDVPPTMAVKFLGACTAACFADLVTP	PLOTAKVRQLQIICGENQ-AVQTARLVQY	58

SfUCPA	57	RGLLTGTIAAREEGSALWKGRIVPGCLRIGLYEPVKSFTYVG--DNFTVGDIP	114	
SfUCPB	57	RGMILGTVAATIAREEGSALWKGRIVPGCLRIGLYEPVKSFTYVG--DNFTVGDIP	114	
StUCP	60	RGLLGTVGTLAKEEGTLWKGGRIVPGCLRIGMYEPVKNLYVG--KDHTVGDVP	117	
AtPUMP	58	RGLLGTVGTLAREEGLRSLWKGGRIVPGCLRIGMYEPVKNLYVFTGKDFVGDVP	117	
human UCP1	56	KGVLTGTTAVVKTEGRKKLYSGLPAGLQRQISSASLRIGLYDTVQEFLTA---GKETAPS	112	
human UCP2	60	RGVMTGTTLMVRTEGRSLYNGLVAGLQRQMSFAASVTRIGLYDSVKQFYT---KGSEHAS	115	
human UCP3	59	RGVLTGTTLMVRTEGRCSPYNGLVAGLQRQMSFAASIRIGLYDSVKQVYTP---KGADNSS	115	

Fig.3 Middle

		III	IV	V
SfUCPA	115	LSRKILLAGLITGALAITVANPTDLVKVRQSEGKLP PG--VPRRYSGALLNAY--STIVRKE	171	
SfUCPB	115	LSRKILLAGLITGALAITVANPTDLVKVRQSEGKLP PG--VPRRYSGALLNAY--STIVRKE	171	
StUCP	118	LSRKILLAGLITGALGITIANPTDLVKVRQAECKLIPAG--VPRRYSGALLNAY--STIVRQE	174	
AtPUMP	118	LSRKILLAGLITGALGIMVANPTDLVKVRQAECKLIAAG--APRRYSGALLNAYFTSTIVRQE	176	
human UCP1	113	LGSKKILLAGLITGGVAATIGOPTEVVKVRQAQSHLHG--IKPRYTGTYNAY--TRIATE	168	
human UCP2	116	IGSRILLAGSTTGALAVAVAQPTDVKVRFQAQARAG---GGRRYQSTVNAY--KTLAREE	170	
human UCP3	116	LTTRILAGCTTGAMAVTCAQPTDVKVRFQASIHLGPSRSDRKYSGTMDAY--RTLAREE	173	
	***
SfUCPA	172	GIGALKITGLGPNTIARNAIINAAELASIDQVTKQTILKLGFSNDNIFTILAG--LGAGFFA	229	
SfUCPB	172	GIGALKITGLGPNTIARNAIINAAELASIDQVVKQ-----	203	
StUCP	175	GVRAALKITGLGPNTIARNAIINAAELASIDQVKEAVLRIPGFTDNVVTHILAG--LGAGFFA	232	
AtPUMP	177	GVRAALKITVLPGPNVARNAIINAAELASIDQVRETIILKIPGFTDNVVTHILSGLFTGAGFFA	216	
human UCP1	169	GLTCGLWKGTTPNLMRSVIINCTELVTYDLMKEAFVKNNILADDVPCHLVSA--LLAGFFCA	226	
human UCP2	171	GFRGLWKGTTSPNVARNAIINCAELVTYDLIKDALLKANLXTOODLPCHFTSA--FGAGFFCT	228	
human UCP3	174	GVRGLWKGTTPNIMRNAIVNCAEVVTYDILKEKLLDYHLLTONFPCFVSA--FGAGFFCA	231	
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Fig.3 Down

VI

SfUCPA 230 VCIGSPVDDVKTRKMSRQKGS---AYRKSTIDCFIRKLKNDGLLAFYKGFIPIMFRLG---SWNVI 285
 SfUCPB 204 -----MKSRQKGS---AYRKSTIDCFIRKLKNDGP LAFYKGFIPIMFRLG---SWNVI 250
 StUCP 233 VCIGSPVDDVKTRKMSRQKGS---AYRKNTIDCFVTKTLKNDGPLAFLYKGFIPIMFRLG---SWNVI 288
 AtPUMP 237 VCIGSPVDDVKTRKMSRQKGS---AYRKGTIDCFVTKTLKSDGPMASFYKGFIPIMFRLG---SWNVI 295
 human UCP1 227 TAMSSPVDPVVKTRKMSRQKSVPPGQYKSVPPGQYKSVPPGQYKSVPPGQYFS2LDCMIKVAQECPТАFYKGFTPSFLRLG---SWNVI 284
 human UCP2 229 TVVAPSPVDPVVKTRKMSRQKSVPPGQYFS2LDCMIKVAQECPТАFYKGFTPSFLRLG---SWNVV 286
 human UCP3 232 TVVAPSPVDPVVKTRKMSRQKSVPPGQYFS2LDCMIKVAQECPТАFYKGFTPSFLRLG---SWNVV 289

PNBD

SfUCPA 286 MFTLITLEQVRKFIFIKEVPN----- 303
 SfUCPB 251 MFTLITLEQVRKFIFIKEVPN----- 268
 StUCP 289 MFTLITLEQAKKVFVKSLESP----- 306
 AtPUMP 296 MFTLITLEQAKKVFVREIDASKRN-- 116
 human UCP1 285 MFTVCFFEQLKRELSKSRQTHDCAT 307
 human UCP2 289 MFTVTTYEQLKRALMACTSREAPP 109
 human UCP3 290 MFTVTTYEQLKRALMVKQMLESPPF 312

Fig.4

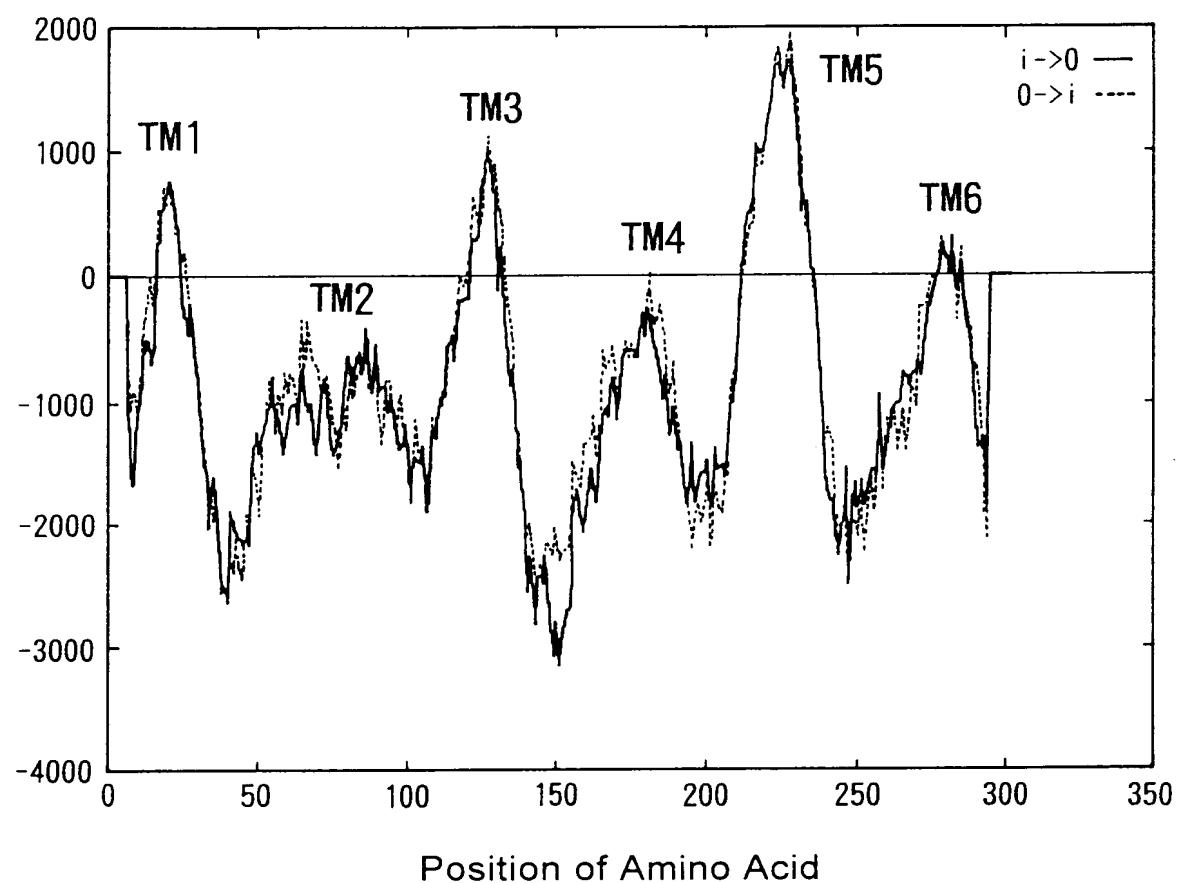


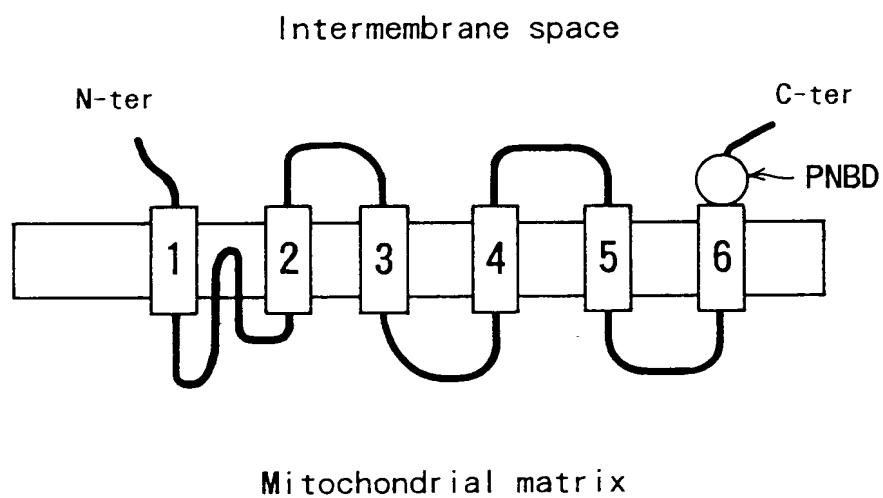
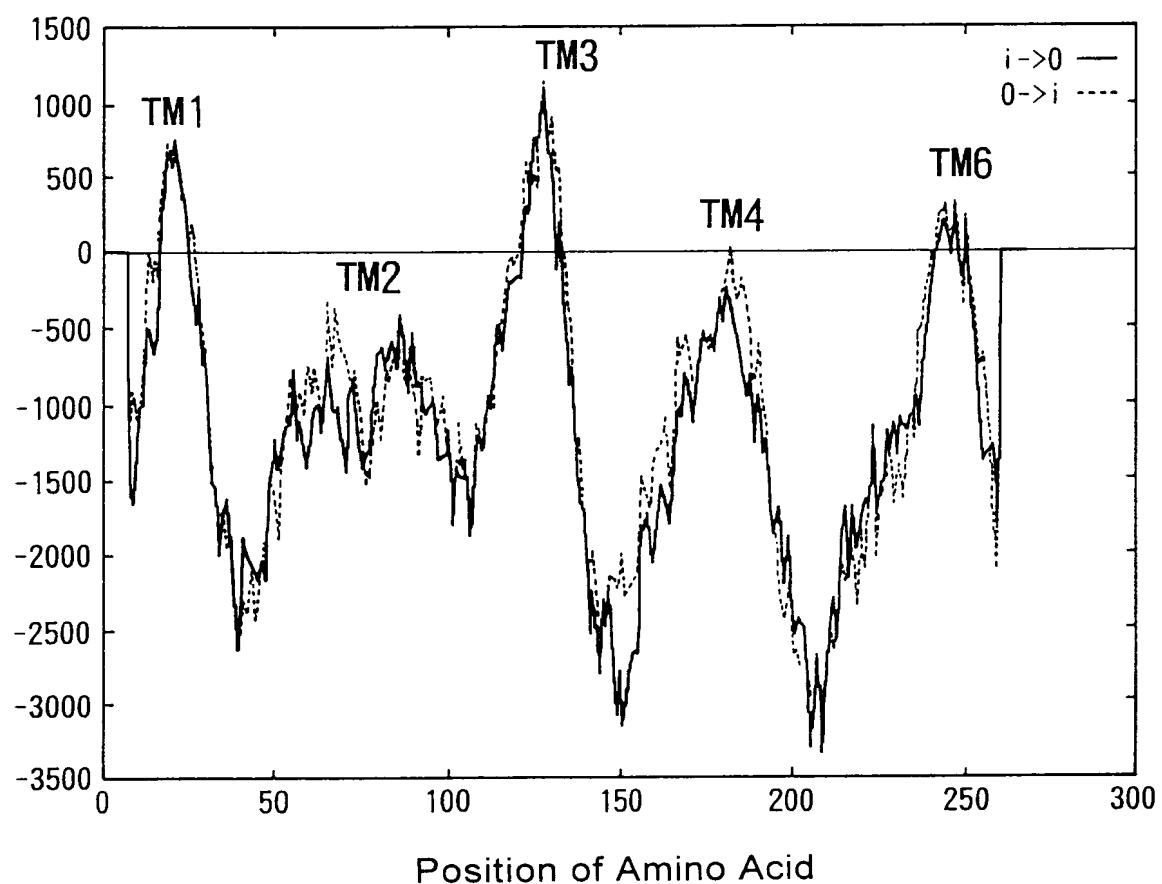
Fig.5

Fig.6



Position of Amino Acid

Fig. 7

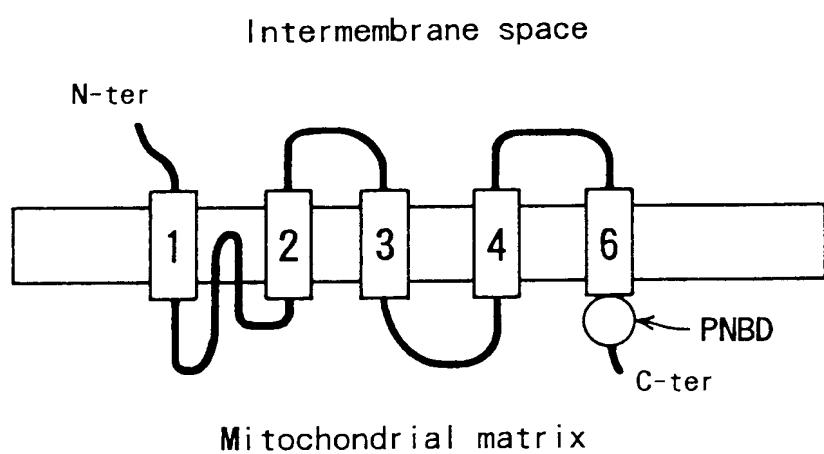


Fig.8